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Fig-1

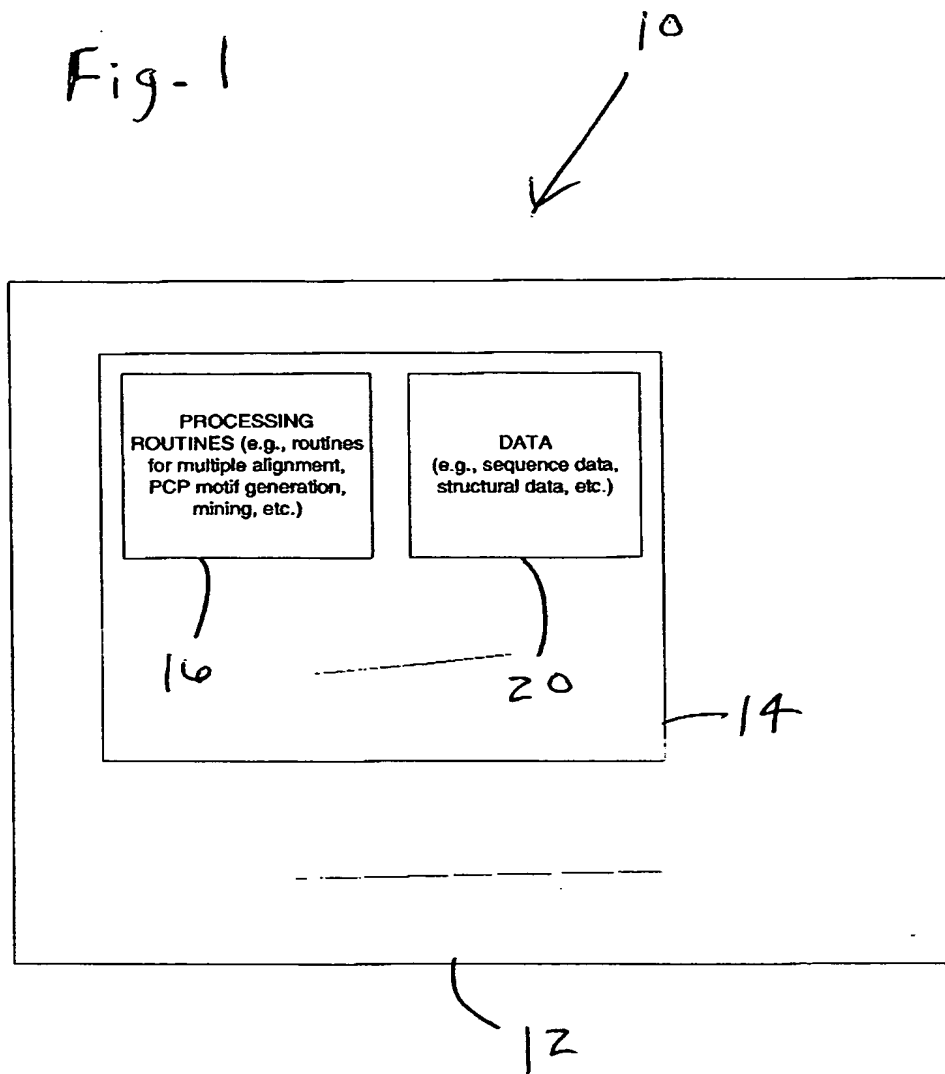
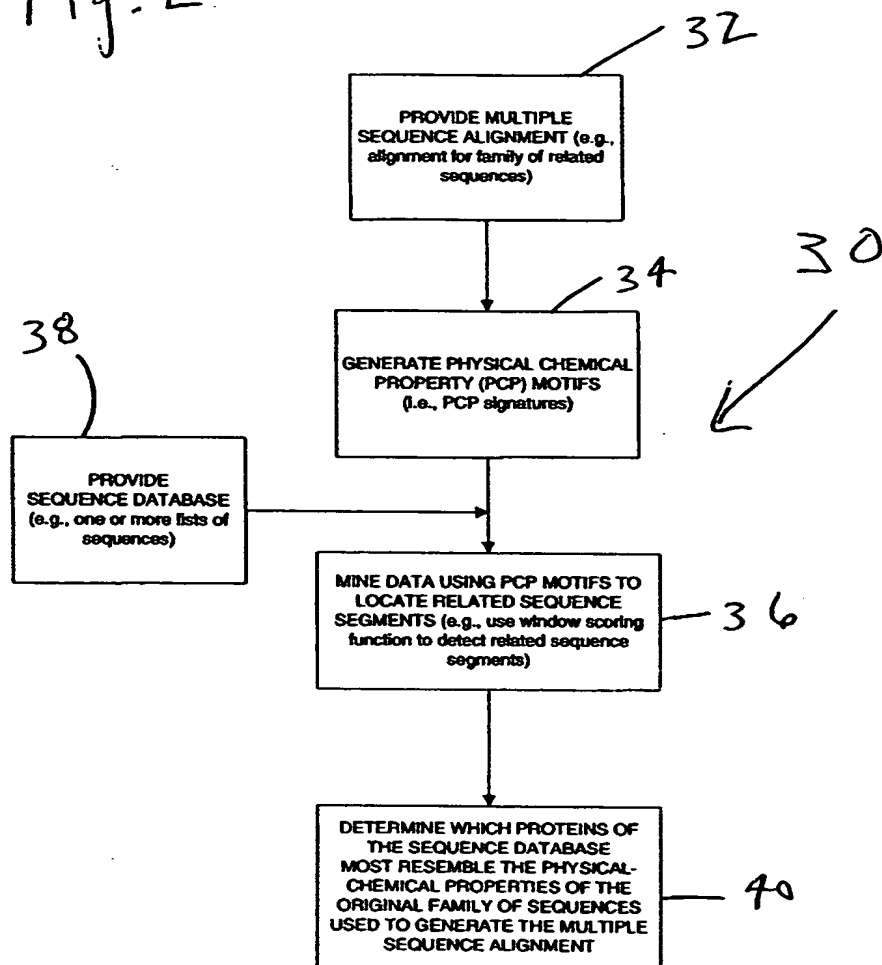


Fig. 2



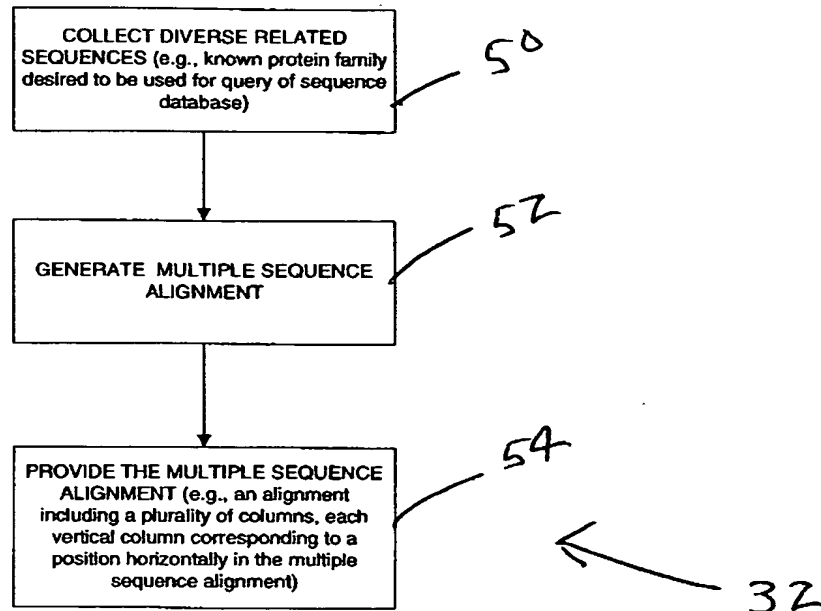


Fig. 3

Fig. 4

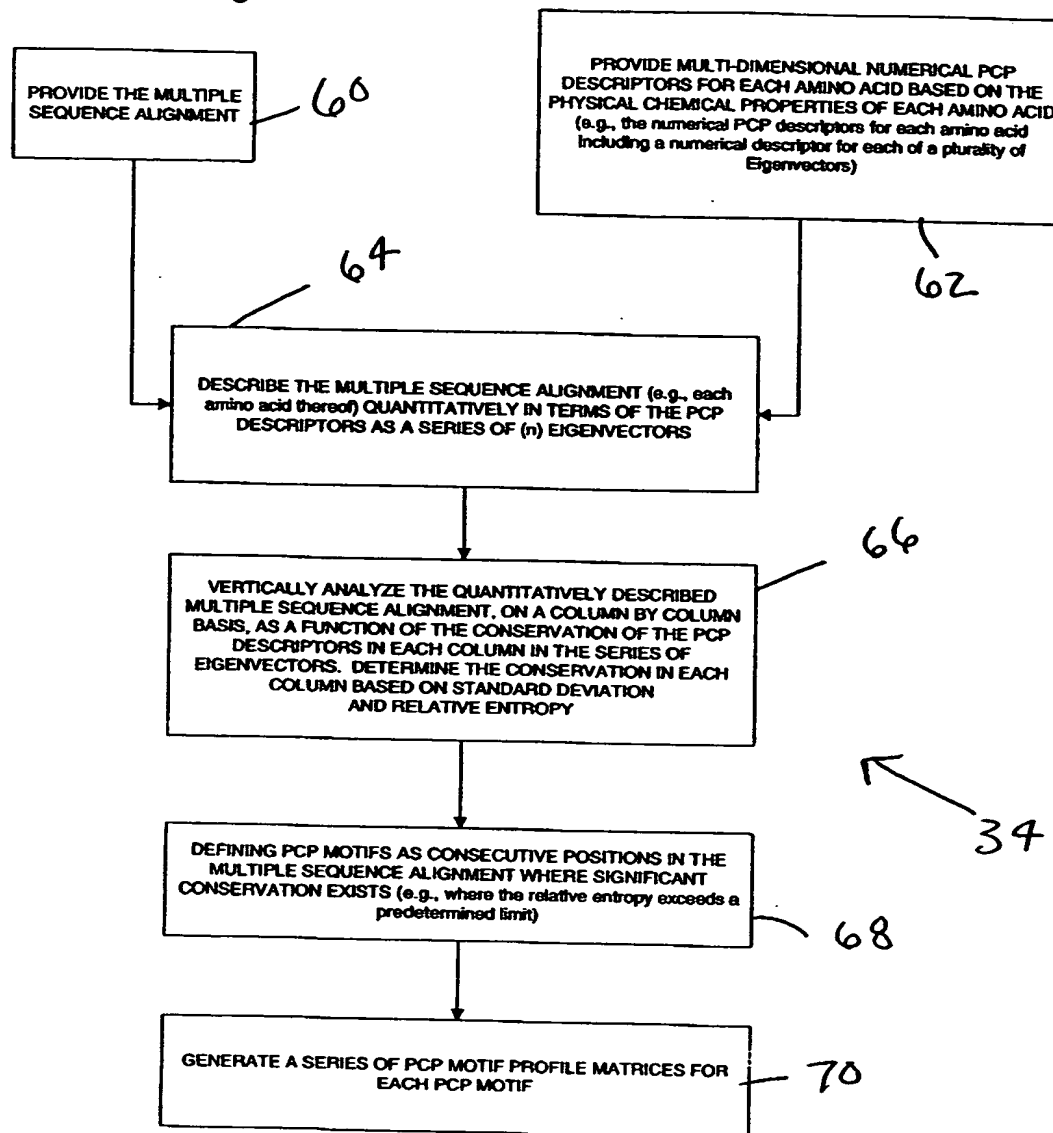


Fig. 5

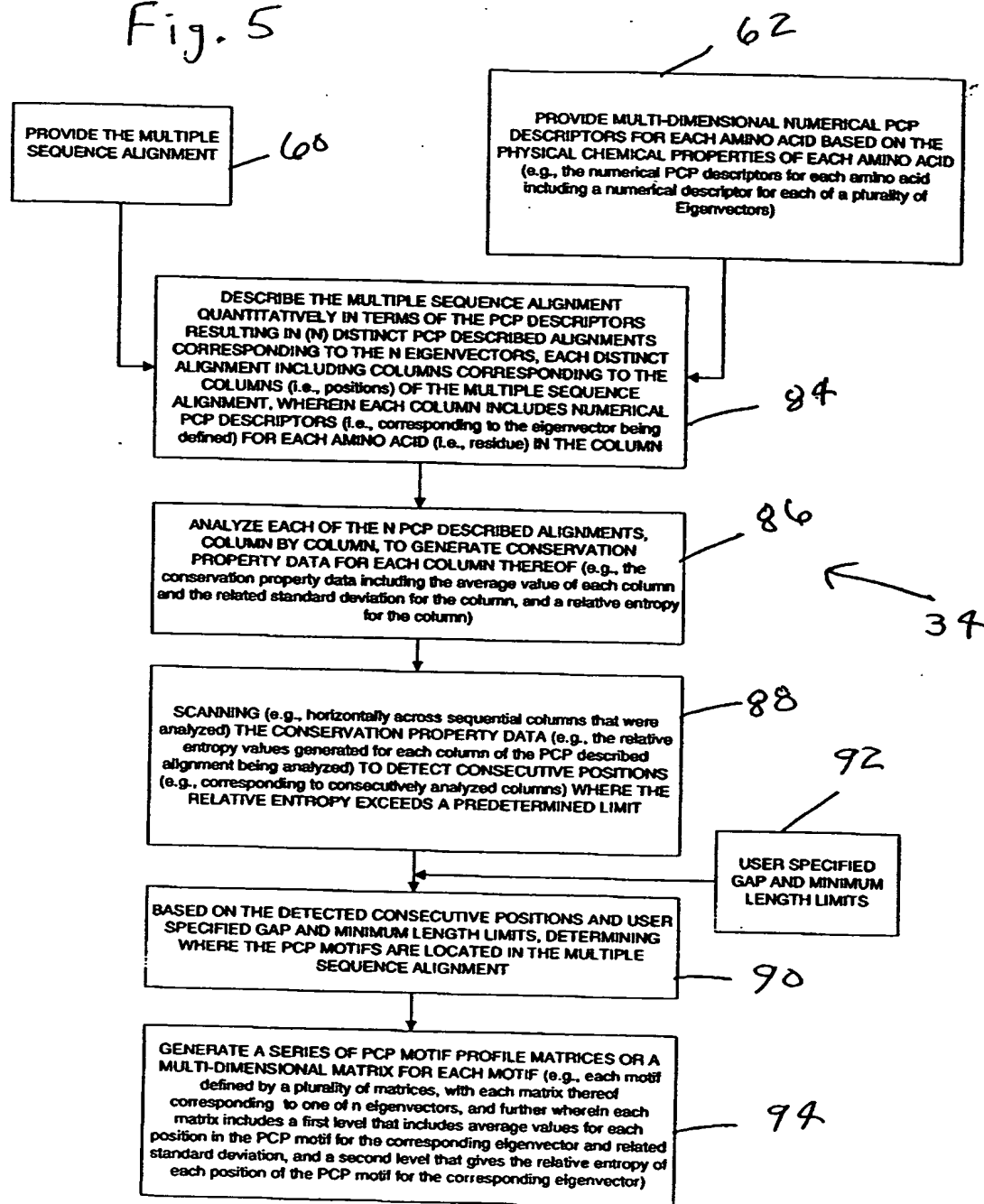


Fig. 6

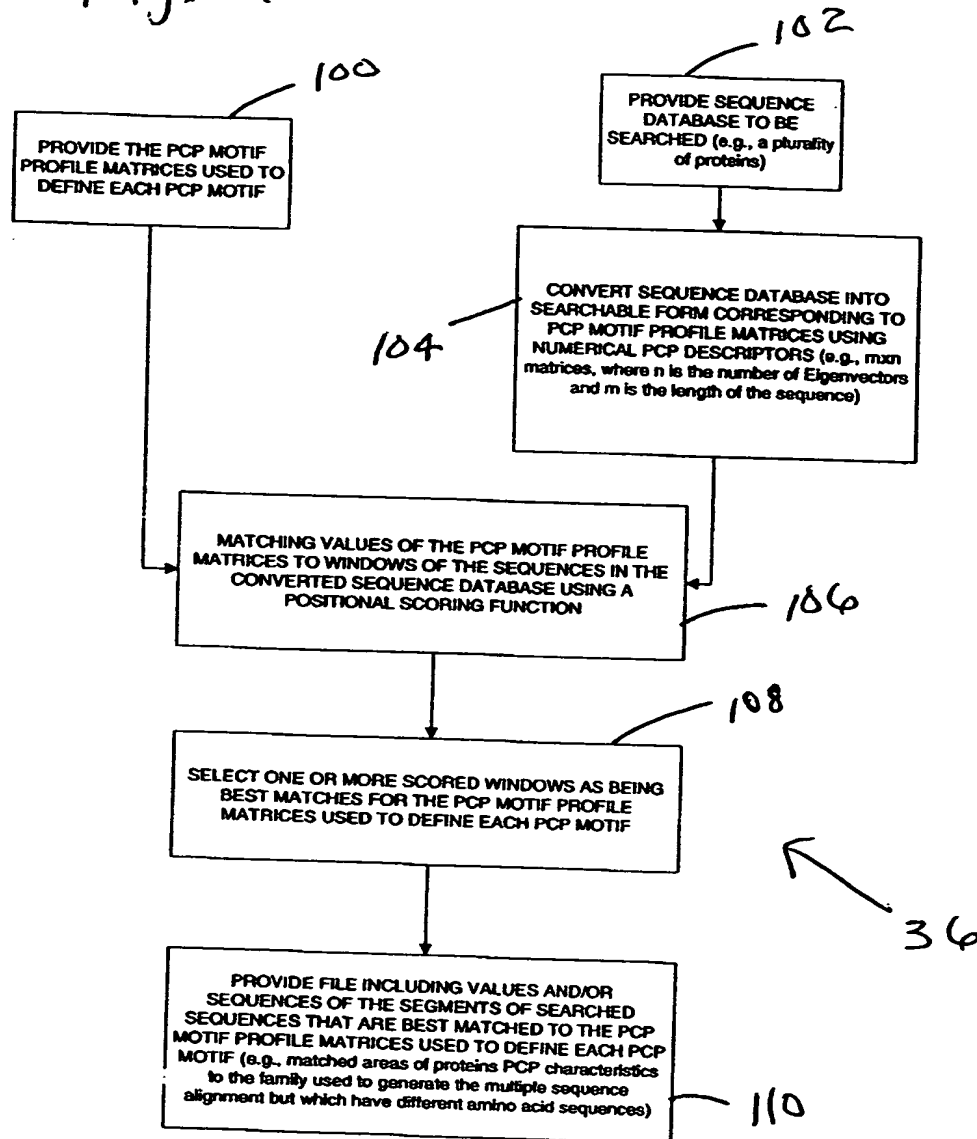


Fig. 7

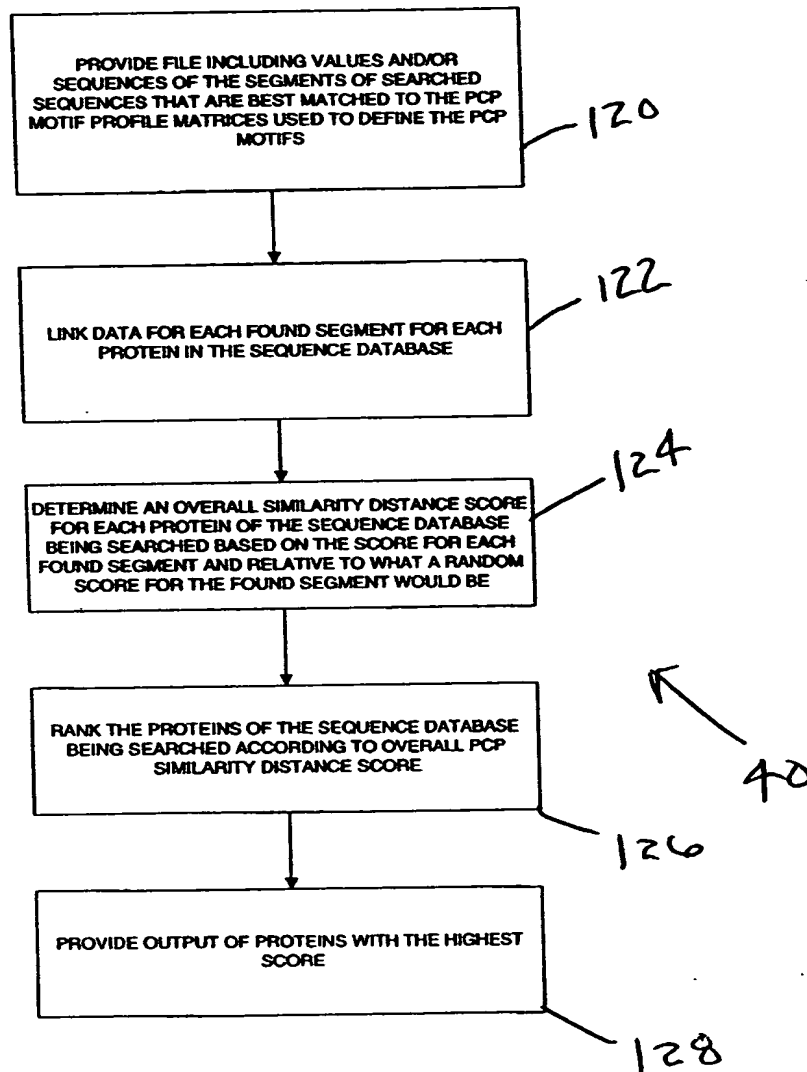
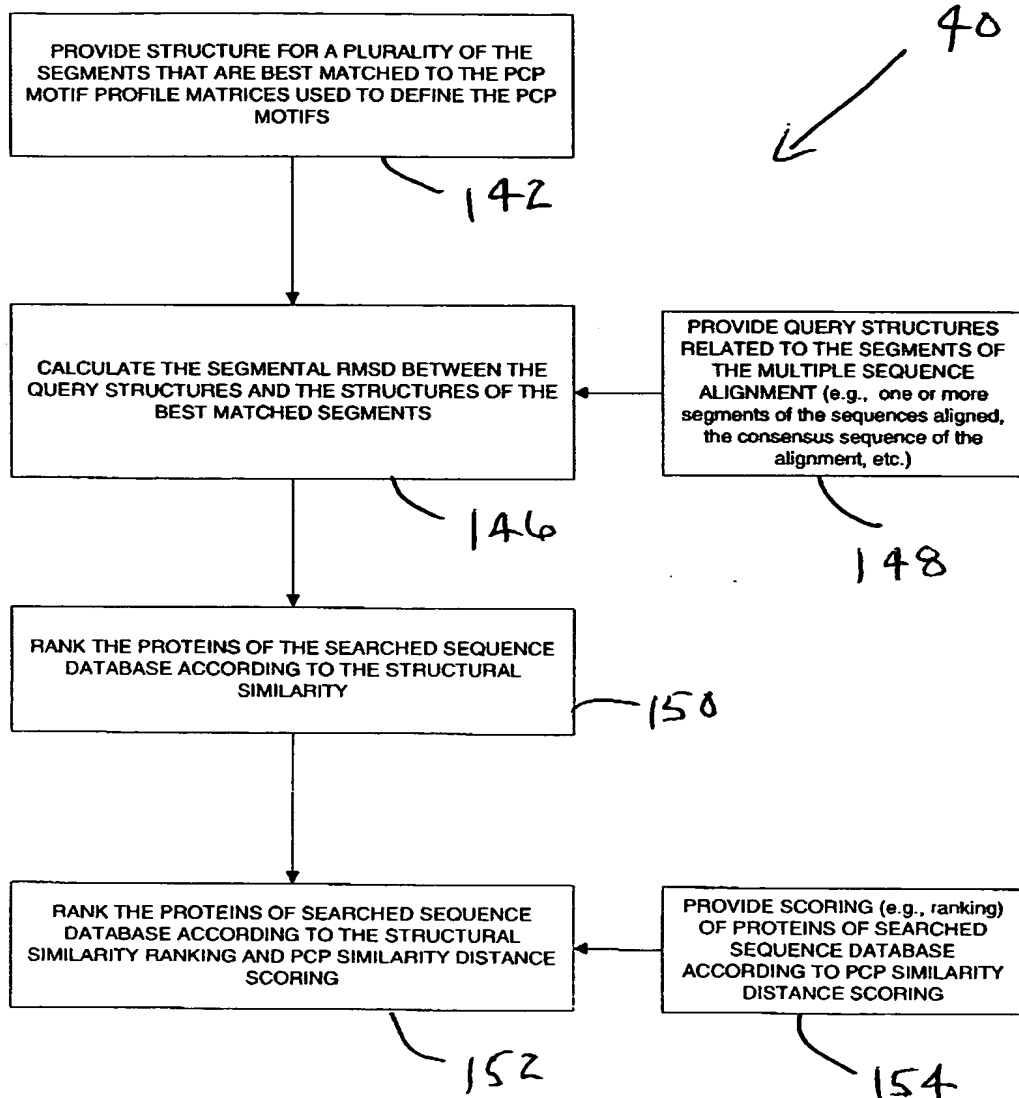


Fig. 8



Motif No.	Query sequence (human APE)	(S1)	(S2)	(S3)	(S4)	42 APE score ave. \pm std. dev	ASTRAL40 ave. \pm std. dev
1	62 LKICSWNVVDGLRA 74	0.91*	0.90*	0.63*	0.73*	0.87 \pm 0.05	0.56 \pm 0.05
2	89 PDILCLQETK 98	0.96*	0.93*	0.84*	0.70*	0.92 \pm 0.04	0.61 \pm 0.07
3	125 KEGYSGVGLSRQP 139	0.91*	0.86*	0.60	0.66	0.85 \pm 0.06	0.64 \pm 0.05
4	145 GIGDEBHDQEGRVIVAEFDSFVL 169	0.94*	0.77*	0.71	0.81	0.84 \pm 0.09	0.67 \pm 0.07
5	171 YVPNA 175	0.96*	0.96*	0.68	0.86	0.94 \pm 0.06	0.68 \pm 0.13
6	181 RLEYRQRW 188	0.80*	0.70*	0.78	0.77	0.74 \pm 0.06	0.67 \pm 0.05
7	204 PLVLCGDLNVAH 215	0.96*	0.88*	0.82*	0.78*	0.90 \pm 0.04	0.55 \pm 0.08
8	231 GFTPQERQFGEL 243	0.96*	0.91*	0.78	0.73	0.87 \pm 0.09	0.70 \pm 0.07
9	247 VPLADSR 254	0.96*	0.93*	0.70	0.83	0.91 \pm 0.08	0.74 \pm 0.11
10	264 YTFWTYM 270	0.86*	0.77*	0.61	0.70	0.84 \pm 0.08	0.61 \pm 0.06
11	274 RSKNVGWRLDYFLLSHSL 291	0.92*	0.89*	0.56	0.64	0.90 \pm 0.04	0.54 \pm 0.07
12	306 GSDHCP 312	0.93*	0.94*	0.88*	0.83*	0.92 \pm 0.03	0.52 \pm 0.09

Fig. 9A

PDB	Score in bits (fraction to the highest score)	Motifs found	SCOP ¹	EC ²	Description
IHD7	1942 (1.00)	1,2,3,4,5,6,7,8,9,10,11,12	d.151.1.1	4.2.99.18	APE
IAGO	1861 (0.96)	1,2,3,4,5,7,8,9,10,11,12	d.151.1.1	3.1.11.2	Exonuclease III
2DNJ	1094 (0.56)	2,6,7,12	d.151.1.1	0.0.0.0	Deoxyribonuclease I
119Y	1056 (0.54)	1,4,5,6,7,9,12	d.151.1.2	0.0.0.0	Phosphatidylinositol phosphate Synaptojanin
1B3U	840 (0.43)	5,7,9,12	a.118.1.2	0.0.0.0	Regulatory domain of protein phosphatase
IMDA	814 (0.42)	6,9,11,12	b.69.2.1	1.4.99.3	Methylamine dehydrogenase
IMPY	797 (0.41)	7,9,12	d.32.1.3	1.13.11.2	Catechol 2,3-dioxygenase
IEKM	792 (0.41)	6,7,12	b.30.2.1	1.4.3.6	Copper amine oxidase
1YRG	737 (0.38)	2,9,12	c.10.1.2	0.0.0.0	Gpase RNAI
1QQ9	698 (0.36)	5,6,12	c.56.5.4	3.4.11.-	Aminopeptidase

¹SCOP code and d.151.1 is the DNaseI superfamily code

²Enzyme commission classification number

Fig. 9B

PDB ¹	Score in bits (fraction to the highest score)	MOLEGOS found	SCOP ²	EC ³	Description
1HD7	1942 (1.00)	1,2,3,4,5,6,7,8,9,10,11,12	d.151.1.1	4.2.99.18	APB (Mn/Mg/Pb)
1AKO	1831 (0.94)	1,2,3,5,6,7,8,9,10,11,12	d.151.1.1	3.1.11.2	Exonuclease III
2DNJ	1072 (0.55)	1,2,5,6,7,9,10,12	d.151.1.1	3.1.21.1	Deoxyribonuclease I
119Y	971 (0.50)	1,2,5,6,7,9,10,12	d.151.1.2		Phosphatidylinositol phosphate Synaptotagmin
1QQ9	698 (0.36)	5,6,9,10,12	c.56.5.4	3.4.11.-	Aminopeptidase (Zn, Ca)
1ATL	633 (0.33)	5,6,9,10,12	d.92.1.9	3.4.24.42	Snake venom metalloprotease (Zn, Ca)
1D09	619 (0.32)	5,9,12	d.58.2.1	2.1.3.2	Aspartate carboxyltransferase (Zn)
1D2N	613 (0.32)	5,6,8,9,12	c.37.1.13		N-ethylmaleimide of sensitive fusion protein (Mg)
1D0B	579 (0.30)	2,5,9,12	c.10.2.1		InternalinB LRR domain (Ca)
1EBM	571 (0.29)	5,6,8,12	a.45.1.1		Glutathione S-transferase
PDB code of the protein					

²SCOP code and d.151.1 is the DNaseI superfamily code

³Enzyme commission classification number

Fig- 9c

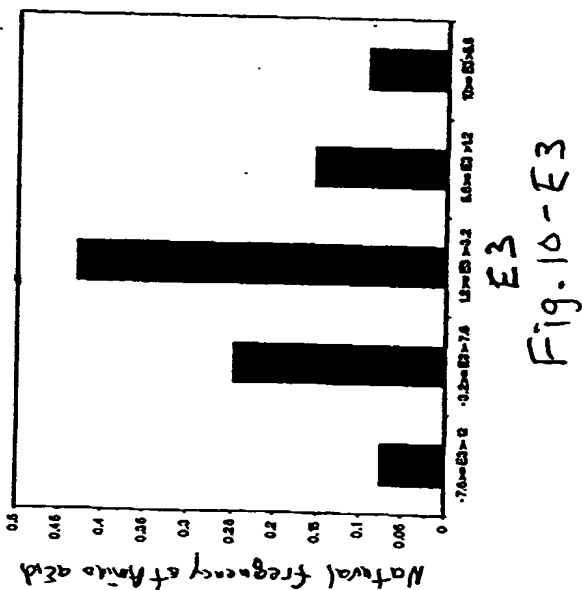
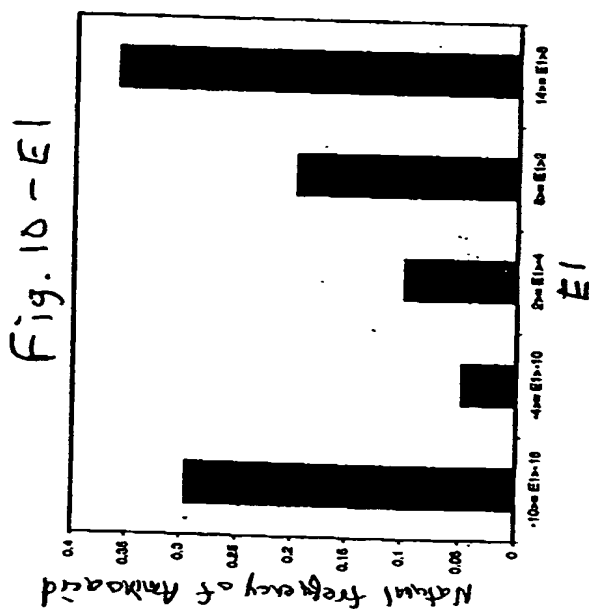
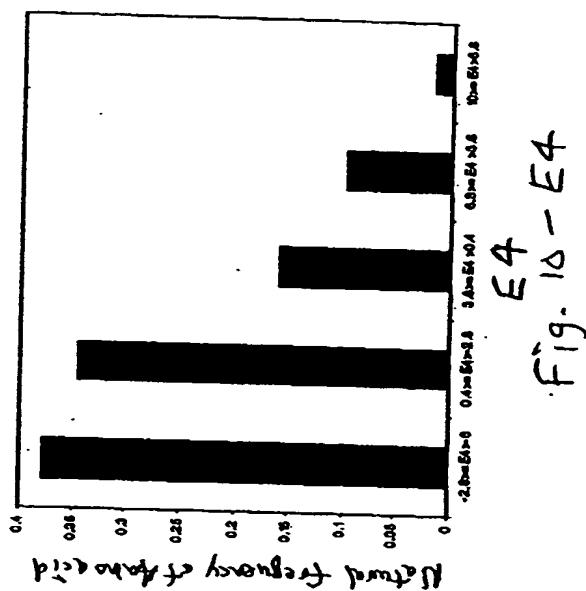
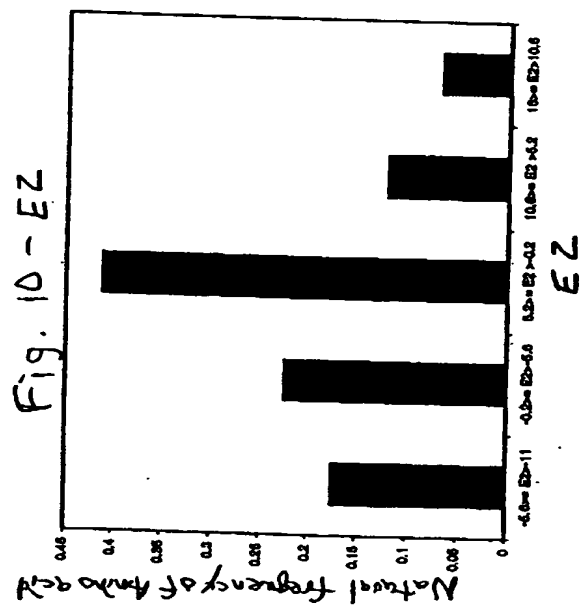
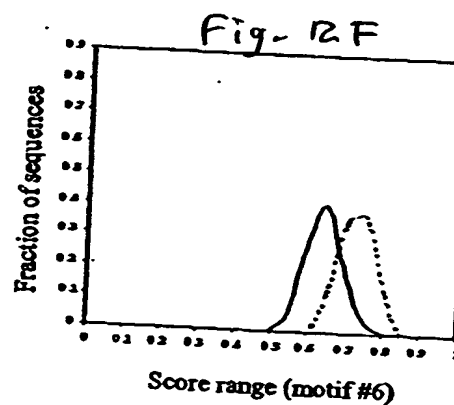
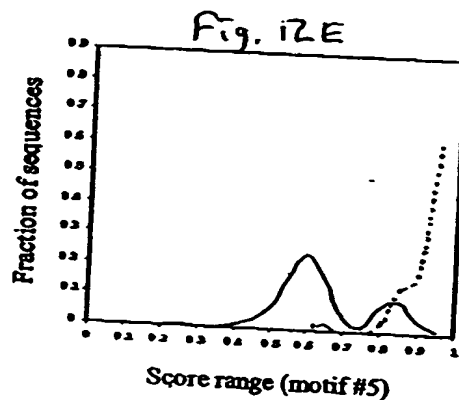
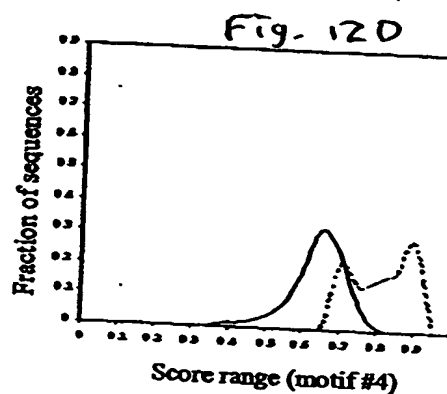
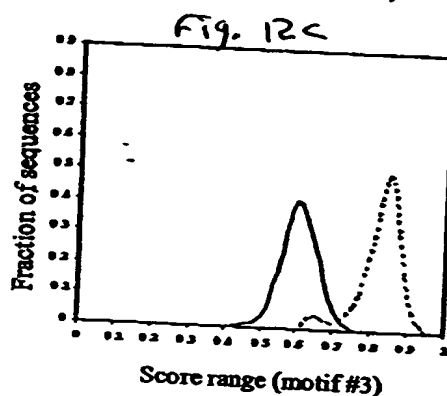
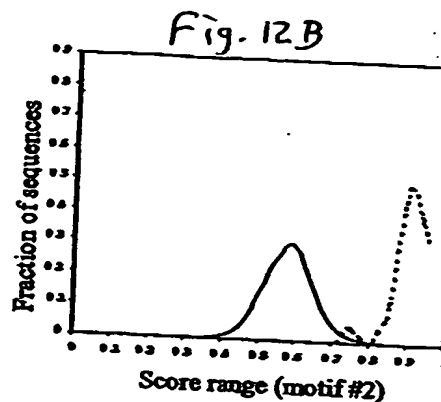
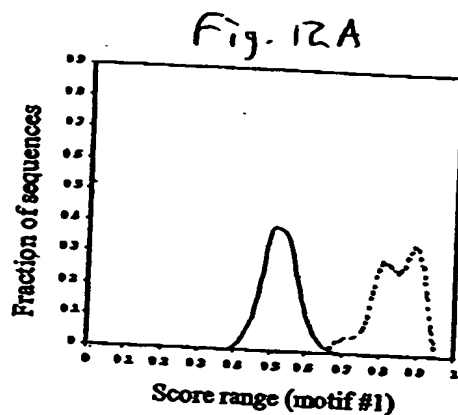
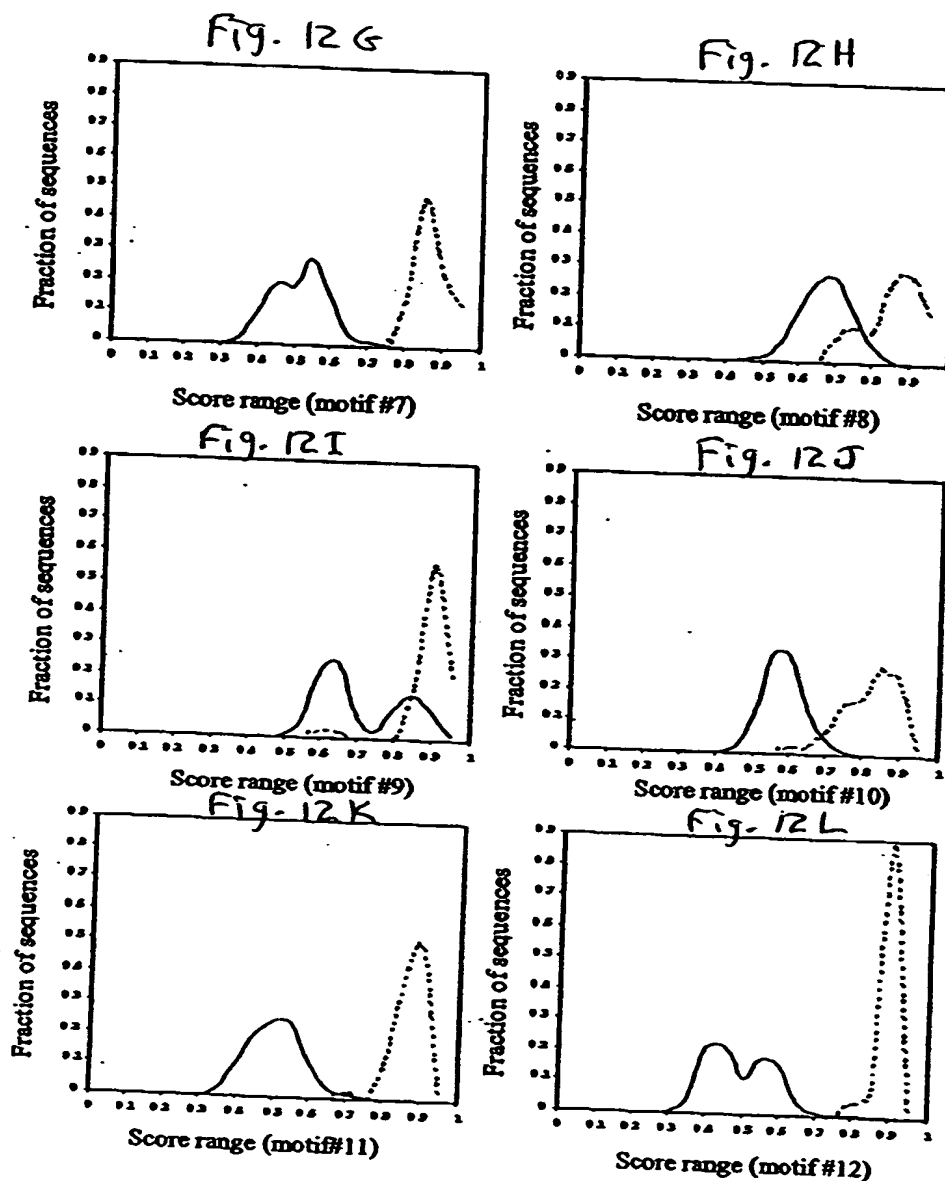


Fig. 11

	P	D	I	L	C	L	Q	E	T	K
E1	*	+	-	-	-	-	+	+	*	*
E2	*	-	*	*	*	*	-	-	*	-
E3	+	*	*	*	*	*	*	-	*	*
E4	*	+	*	*	+	*	+	+	*	-
E5	*	+	*	*	*	*	-	+	*	-





1
1bixLIEDPFDQRTSPSGKPA...LKICSNHVDGLRAW.....IKKGLDNVKE.ZA
1akoHMFVPSFMINGLAR.....P..HOLKAIVAGHQ
3dniLKTAAFWIRTFGCKmsnatLASTIVR...R
119ya ydphayvnhelkrenefseKRWV...IFVASTHNG..CS.....ATTK.LEHMLF.Po

2
1bix P.....DILCLQSTK.....CSERKL.P..AKLOEL.....PGLSHQIWS.APSD
1ako P.....DVIGLQSTK.....VHDDMF.P.LEVAKL.....G..INVFYH.G...
3dni K.....DIVLIGEVF.....DSHLVAVG..KLDDTL.....nqddpHTH.YVBSaFLGR
119ya HtPladiYVVGQHIValtSADPAkreweSCVAKllngkctsupgIVQLRSCQL.V...

3
1bix KEGTSGVCLLR...QCP.....LEVSXIGDE....KEDQE.GRVIVAEFD....
1ako QCHIGVALLTK...RTF.....IAVERGTFGD.....DKKQGRITMAKIP.....sl
3dni nSTKRYLFLFapakVSV.....LDITQ.YDDGccgmdSFER..EPAVVKFSahstk
119yaGTALHF...ChesolpeiknveOTVAK.....tGLGR.KCAVAIRFD....ye

4
1bix ..SFVLVTAYVPHAGGLV...KLSTQGMOKAFKYLEG.....LA...S.RK...PLVL
1ako lgvTVINGTFPQGRSDHPKFFPAKQFPQMLWLET.....KL...KIDN...PVLY
3dni vKFAIVALSAPS.....DAVAKDESLLIVILD.....VQqwh.LN.DVHL
119ya dtGLCTITSELANGY.....TWDERORDVITIASglfrgrSI...P.MHIVVW

5
1bix ..GGLVVAHEKIDLEN....PACBK..KRCGTFPQ.....KRCQF
1ako SCIDHLSPLDLDIGIGeeKHRLtGRCSVLPE.....ERENH
3dni KCDVHAD.....CSVITS.....QWSS.
119ya KCDVHY.....RISLtyeevpciaqklsyifeydqlKRCM

6
1bix G..KLQAVPLADSPRLYPPTFYATTWTY..MMHARSKW...GGLDYFLLSES..LL
1ako D..RLMSW.GLVDTIKRANPQTADSFMDY..RSGFDONR...GLRIDELLASQP.LA
3dni I..KLRTSTFQMLIP.....GSADTYAT.....ST..NCAYDIRIVVAGSILQ
119ya LtgKVPF..FFSELPY.....tFPTTKFDigtDITDTSdkhrvPANTDMLLYRGE.L.

7
1bix PALC..DSKIRSKA.....L...SDHCP...FLYLAL
1ako ECCV..ETGIDYK.....RemehPSGAPWATFX.....
3dni SSVVpgsAAFFDPQayplscnemaL...ISDHYFVEVLZ.
119ya .VPH..STQSP.PL.....Y...TSDHPTATTEanivkvdrckkilfeol

8
1bix
1ako
3dni
119ya ynaqkqevrdnag

Fig. 14

